

GenCore version 4.5
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OM protein - protein search, using sw model

Run on:

March 1, 2001, 16:09:16 ; Search time 299.73 Seconds
(without alignments)

24.636 Million cell updates/sec

Title: US-09-331-631A-3_COPY_186_248

Perfect score: 353

Sequence: 1 KRDPOQREYEDCRRCEQQE.....LINPQRGGSGRYERGEEKOS 63

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_15 *

- 1: sp_arched:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rordan:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	353	100.0	666	10	Q9SPFL4
2	334	94.6	625	10	Q9SPFL3
3	332	94.1	666	10	Q9SPFL5
4	125.5	35.6	593	10	Q9SEW4
5	118.5	33.6	525	10	Q43358
6	103	29.2	637	10	Q03678
7	89.5	25.4	810	10	Q9ZWL3
8	85.5	24.2	1483	5	Q9yD46
9	84	23.8	236	10	Q81254
10	82	23.2	630	5	Q9W4J3
11	81	22.9	242	10	Q81251
12	81	22.9	242	10	Q9SB6
13	81	22.9	539	4	Q9NUA2
14	80	22.7	238	10	Q81257
15	80	22.7	393	10	Q9ZTP0
16	79	22.4	238	10	Q81258
17	79	22.4	238	10	Q9SB5
18	79	22.4	238	10	Q9SB6
19	79	22.4	242	10	Q9SBZ6
20					tripsacum d

Database : Q9SPFL3

Title: SPTREMBL_15 *

1

RESULT 1
Q9SPFL4 PRELIMINARY; PRT; 666 AA.

ID Q9SPFL4; AC Q9SPFL4; DT 01-MAY-2000 (TRIMBREL. 13, Last sequence update)
DT 01-MAY-2000 (TRIMBREL. 13, Last annotation update)
DT 01-OCT-2000 (TRIMBREL. 15, Last annotation update)
DE VICTILIN PRECURSOR.

AMP2.

GN Macadamia integrifolia (Macadamia nut).

OC Eukaryota; Viriplantae; Embryophyta; Tracheophyta; Spermatophyta;

OC Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.

OX NCBI_TaxID=6098; RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=NUT KERNEL;

RA Marcus J.P., Goultier K.C., Green J.L., Manners J.M.;

RT "A family of antimicrobial peptides is produced by processing of a 7S

RT globulin protein in Macadamia integrifolia.";

PLANT J. 0:0-0(1999).

EMBL; AF161884; AAD4245.1; -.

DR HSSP; P0253; 2PBL.

DR INTERPRO; IPR001113; -.

DR PFAM; PF00546; Seedstore_7s; 1.

DR SEQUENCE 666 AA; 78243 MW; 0ECN22F8710F8A7B CRC64;

Query Match Best Local Similarity 100.0%; Score 353; DB 10; Length 666; Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q9vd46 drosophilila
Q81254 zea mays su
Q9W4J3 drosophilila
Q81251 zea mays su
Q9SB6 zea mays su
Q9NUA2 homo sapien
Q81257 zea luxuria
Q9ZTP0 oryza sativa
Q81258 zea luxuria
Q9SB5 zea luxuria
Q9SB6 zea luxuria
Q81260 tripsacum d

ALIGNMENTS

20	79	22.4	246	10	Q81261 triplasacum d
21	78.5	22.2	1655	5	Q24754 drosophila
22	78	22.1	240	10	Q81252 zea mays su
23	78	22.1	240	10	Q9SBF0 zea mays su
24	78	22.1	240	10	Q9SBF9 zea mays su
25	78	22.1	240	10	Q9SBF7 zea mays su
26	78	22.1	411	5	P91419 caenorhabdil
27	78	22.1	540	10	Q03866
28	77	21.8	238	10	Q81255 zea mays su
29	76.5	21.7	296	10	Q95709 arabiopsis su
30	76.5	21.7	128	5	Q9VZ60 drosophila
31	75.5	21.4	239	10	Q9SBF1
32	75.5	21.4	556	0	Q9SBF1 zea mays su
33	75.5	21.4	663	5	Q9W352 drosophila
34	75	21.2	562	5	Q9U345 caenorhabdil
35	75	21.2	568	5	Q9U344 caenorhabdil
36	75	21.2	5	0	Q9vgs7 dictyosteli
37	74.5	21.1	238	10	Q81249 zea mays su
38	74.5	21.1	238	10	Q9SBF8 zea mays su
39	74.5	21.1	407	10	Q41750 zea mays (m
40	74.5	21.1	582	10	Q03865 zea mays (m
41	74.5	21.1	686	5	Q45255 caenorhabdil
42	74.5	21.1	1309	5	Q9vde9 drosophila
43	74	21.0	236	10	Q81250 zea mays su
44	74	21.0	236	10	Q9SBF2 zea mays su
45	74	21.0	236	2	Q9sbff2 zea mays su
46	21.0	206	0	0	Q87306 borrelia bu

ID	Q9SP3	PRELIMINARY;	PRT;	625 AA.
AC	Q9SP3;			
DT	01-MAY-2000 (TREMBLrel. 13, last sequence update)			
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)			
DE	VICILIN PRECURSOR (FRAGMENT), AMP2.			
GN	Macadamia integrifolia (Macadamia nut).			
OS	Macadamia integrifolia (Macadamia nut).			
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;			
OC	Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.			
OX	NCBI_TaxID=6098;			
RN	[1] -SEQUENCE FROM N.A.			
RP	TISSUE=NUT KERNEL;			
RC	Marcus J.P., Goultier K.C., Green J.L., Manners J.M.;			
RA	"A family of antimicrobial peptides is produced by processing of a 7S globulin protein in Macadamia integrifolia.";			
RT	Plant J. 0:0-0(1999).			
RL	EMBL: AF161885; AAD54246.1; -.			
DR	HSSP; P02853; 2PBL.			
DR	INTERPRO; IPR001113; -.			
PFAM; PF00546; Seedstore_7s; 1.				
FT	NON_TER			
SEQUENCE	625 AA; 73586 MW; 415508A89D370296 CRC64;			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CV_SUNLAND; TISSUE=SOMATIC EMBRYO LINE;			
RA	Teuber S.S., Jarvis K.C., Peterson W.R., Dandekar A.M., Ansari A.A.;			
AC	"Identification and cloning of a cDNA encoding a vicilin-like protein, Jug r 2, from English walnut kernel (Juglans regia): a major food allergen.";			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)			
DE	VICILIN PRECURSOR.			
GN	AMP2.			
OS	Macadamia integrifolia (Macadamia nut).			
OC	Eukaryota; Viridiplantae; Embryophyta; Spermatophyta;			
OC	Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.			
OX	NCBI_TaxID=6098;			
[1]	SEQUENCE FROM N.A.			
RC	Marcus J.P., Goultier K.C., Green J.L., Manners J.M.;			
RA	"A family of antimicrobial peptides is produced by processing of a 7S globulin protein in Macadamia integrifolia kernels.";			
RT	Plant J. 0:0-0(1999).			
RL	EMBL: AF161883; AAD54244.1; -.			
DR	HSSP; P02853; 2PBL.			
DR	INTERPRO; IPR001113; -.			
PFAM; PF00546; Seedstore_7s; 1.				
FT	NON_TER			
SEQUENCE	593 AA; 69990 MW; 9BA127E19B18C0D8 CRC64;			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CV_SUNLAND; TISSUE=SOMATIC EMBRYO LINE;			
RA	Teuber S.S., Jarvis K.C., Peterson W.R., Dandekar A.M., Ansari A.A.;			
AC	"Identification and cloning of a cDNA encoding a vicilin-like protein, Jug r 2, from English walnut kernel (Juglans regia): a major food allergen.";			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)			
DE	VICILIN PRECURSOR.			
GN	AMP2.			
OS	Macadamia integrifolia (Macadamia nut).			
OC	Eukaryota; Viridiplantae; Embryophyta; Spermatophyta;			
OC	Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.			
OX	NCBI_TaxID=6098;			
[1]	SEQUENCE FROM N.A.			
RC	Marcus J.P., Goultier K.C., Green J.L., Manners J.M.;			
RA	"A family of antimicrobial peptides is produced by processing of a 7S globulin protein in Macadamia integrifolia kernels.";			
RT	Plant J. 0:0-0(1999).			
RL	EMBL: AF161883; AAD54244.1; -.			
DR	HSSP; P02853; 2PBL.			
DR	INTERPRO; IPR001113; -.			
PFAM; PF00546; Seedstore_7s; 1.				
FT	SEQUENCE	666 AA; 78217 MW; C752B884B2DF0224 CRC64;		
RP	SEQUENCE FROM N.A.			
RC	THEOBROMA CACAO (Cacao).			
OS	Theobroma cacao (Cacao).			
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;			
OC	Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Theobroma.			
OC	Malvales; Malvaceae; Theobroma.			
OX	NCBI_TaxID=3641;			
[1]	SEQUENCE FROM N.A.			
RC	TISSUE=LEAVES;			
RP	SEQUENCE FROM N.A.			
RC	MEDLINE=92288309; PubMed=1600151;			
RA	McHenry L., Fritz P.J.; "Comparison of the structure and nucleotide sequences of vicilin genes of coca and cotton raise questions about vicilin evolution.";			
RT	Plant Mol. Biol. 18:1173-1176(1992).			
RL	X62625; CAA4493.1; -.			
DR	EMBL: X62625; CAA4494.1; -.			
DR	HSSP; P02853; 2PBL.			

Query Match 94.1%; Score 332; DB 10; Length 666;
Best Local Similarity 92.1%; Pred. No. 7 3e-32;
Matches 58; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 KRDPQOREYEDCRRCEQQEPRQHQCORRCREREQQHQHGRGDLINPORGSGSRVREGEE 60
Db 186 KRDPQOREYEDCRRCEQQEPRQHQCORRCREREQQHQHGRGDLINPORGSGSRVREGEE 245

DR	MENDEL; 30919; THECC;1188;30919.
INTERPRO;	IPR001113; -.
PFAM;	PF0056; Seedstore_7s; 1.
PRODOM;	PD081059; -; 1.
KW	Signal.
FT	SIGNAL
CHAIN	1 24
SEQUENCE	25 AA: 525 MW: 19114CD5C248905D CRC64;
DB	92 CQQQQQ 99
RESULT	6
Q03678	PRELIMINARY; PRT; 637 AA.
AC	Q03678;
DT	01-NOV-1996 (TREMBLrel. 01, Created)
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE	FETAL STORAGE PROTEIN.
GN	BEG1 OR GB1.
OS	Hordeum vulgare (Barley), and Triticum aestivum (wheat).
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC	Magnoliophyta; Liliopsida; Poales; Poaceae; Hordeum.
OX	NCBI_TaxID=4513, 4565;
RN	[1]
RP	SEQUENCE FROM N. A.
RX	MEDLINE=93287938; PubMed=8510647;
RA	Heck G.R., Chamberlain A.C., Ho T.-H.D.;
RT	"Barley embryo globulin 1 gene, Beg1, characterization of cDNA, chromosome mapping and regulation of expression.";
RL	Mol. Gen. Genet. 239:209-218(1993).
DR	EMBL: M64372; AAA32036.1; -.
DR	EMBL: W8119; AAA34369.1; -.
DR	HSSP: P02853; 2PHL.
DR	MENDEL; 8553; Horv1;188;8553.
DR	INTERPRO; IPR000901; -.
DR	INTERPRO; IPR001113; -.
DR	PFAM; PF00546; Seedstore_7s; 1.
DR	PRODOM; PS00847; CQSASE_2; UNKNOWN_1.
DR	PRODOM; PS0081059; -; 1.
KW	Seed storage protein.
SEQUENCE	637 AA; 72252 MW; F323F4FF99947C3C CRC64;
RP	SEQUENCE FROM N. A.
RC	STRAIN-BERKELEY;
RX	BBMLIB=20196006; PubMed=10731312;
RA	Adams M.D., Celinkin S.E., Holt R.A., Evans C.A., Cocayne J.D., Ananatides P.G., Scheier S.E., Li P.W., Hoskins R.A., Galie R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.S., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Peiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews Pfanckoch C., Baldwin D., Bailew R.M., Basu A., Baxendale J., Bayraktaroglu E., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borckova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadile E., Center A., Chandra I., Cherry J.M., Cowley S., Dahlke C., Davenport L.B., Davies P., de Pablo B., Delcher A., Deng Z., Mayes A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin R.K., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W., Fosler C., Gabrielian A.E., Gang N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan J., Harris M.,
RESULT	7
Q9ZW13	PRELIMINARY; PRT; 810 AA.
DR	01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE	PV100.
OS	Cucurbita maxima (Pumpkin) (winter squash).
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids I; Cucurbitales; Cucurbitaceae; Cucurbita.
OC	NCBI_TaxID=3661;
RN	[1]
RP	SEQUENCE FROM N. A.
RC	STRAIN-KUROKAWA AMAKURI NANKIN; TISSUE=COTYLEDON;
RX	MEDLINE=99107919; PubMed=9831029;
RA	Namada K., Shimada T., Kondo M., Nishimura M., Hara Nishimura I.;
RT	"Multiple functional proteins are produced by cleaving Asn-Gln bonds of a single precursor by vacuolar processing enzyme.";
RL	J. Biol. Chem. 274:2563-2570(1999).
DR	EMBL: AB019195; BAA34506.1; -.
DR	HSSP; P02853; 2PHL.
DR	INTERPRO; IPR001113; -.
DR	PFAM; PF00546; Seedstore_7s; 1.
DR	PRODOM; PD081059; -; 1.
SQ	SEQUENCE 810 AA; 97314 MW; A829A3F7542266AB CRC64;
RESULT	8
Q9VDA6	PRELIMINARY; PRT; 1483 AA.
ID	Q9VDA6;
AC	Q9VDA6;
DT	01-MAY-2000 (TREMBLrel. 13, Created)
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE	CG5740. PROTEIN.
GN	Drosophila melanogaster (fruit fly).
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oo-Ephydriidea; Drosophilidae; Drosophila.
OX	NCBI_TaxID=7227;
RN	[1]
RP	SEQUENCE FROM N. A.
RC	STRAIN-BERKELEY;
RX	BBMLIB=20196006; PubMed=10731312;
RA	Adams M.D., Celinkin S.E., Holt R.A., Evans C.A., Cocayne J.D., Ananatides P.G., Scheier S.E., Li P.W., Hoskins R.A., Galie R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.S., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Peiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews Pfanckoch C., Baldwin D., Bailew R.M., Basu A., Baxendale J., Bayraktaroglu E., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borckova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadile E., Center A., Chandra I., Cherry J.M., Cowley S., Dahlke C., Davenport L.B., Davies P., de Pablo B., Delcher A., Deng Z., Mayes A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin R.K., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W., Fosler C., Gabrielian A.E., Gang N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan J., Harris M.,

RESULT 11
 ID 081251 PRELIMINARY; PRT; 242 AA.
 AC 081251;
 DT 01-NOV-1998 (TREMBrel. 08, Created)
 DT 01-OCT-2000 (TREMBrel. 15, Last sequence update)
 OS GLOBULIN-1 (FRAGMENT).
 OC Zea mays subsp. mays (maize).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
 OX NCBI_TaxID=4578;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hilton H., Gaut B.S.;
 RT "Speciation and domestication in maize and its wild relatives:
 evidence from the Globulin-1 gene.";
 RL Genetics 0:0-0(1998).
 EMBL; AF064214; AAC31457.1; -.
 HSSP; P50477; ICAU.
 MENDEL; 31893; Zeaau;1188;31893.
 DR INTERPRO; IPR000901; -.
 DR INTERPRO; IPR00113; -.
 PRAM; PF00546; Seedstore_7s; 1.
 PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
 FT NON_TER 242 AA; 27860 MW; 913912DE924B0ADB CRC64;

RESULT 12
 ID 09SB6 PRELIMINARY; PRT; 242 AA.
 AC 09SB6;
 DT 01-MAY-2000 (TREMBrel. 13, Created)
 DT 01-MAY-2000 (TREMBrel. 13, Last sequence update)
 DT 01-OCT-2000 (TREMBrel. 15, Last annotation update)
 DE GLOBULIN-1 (FRAGMENT).
 OS Zea mays subsp. parviflumis.
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
 OX NCBI_TaxID=76912;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hilton H., Gaut B.S.;
 RT "Speciation and domestication in maize and its wild relatives:
 evidence from the Globulin-1 gene.";
 RL Genetics 0:0-0(1998).
 EMBL; AF064225; AAC31468.1; -.
 HSSP; P50477; ICAU.
 DR INTERPRO; IPR00113; -.
 DR PF00546; Seedstore_7s; 1.
 SQ SEQUENCE 242 AA; 27856 MW; 8E6DB2C9E45C6BAD CRC64;

Query Match 22.9%; Score 81; DB 10; Length 242;
 Best Local Similarity 35.9%; Pred. No. 0/03; Mismatches 18; Indels 16; Gaps 3;

RESULT 13
 ID QNUA2 PRELIMINARY; PRT; 539 AA.
 AC 09NUA2;
 DT 01-OCT-2000 (TREMBrel. 15, Created)
 DT 01-OCT-2000 (TREMBrel. 15, Last sequence update)
 DE DJ8084.1 (ANDROGEN RECEPTOR (DIHYDROTESTOSTERONE RECEPTOR))
 DE (FRAGMENT).
 AR Homo sapiens (Human).
 DR Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 DR NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chapman J.; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AL049564; CAB87955.1; -.
 KW Receptor.
 FT NON_TER 539 AA; 55444 MW; AB493953BB89D869P CRC64;

RESULT 14
 ID 081257 PRELIMINARY; PRT; 238 AA.
 AC 081257;
 DT 01-NOV-1998 (TREMBrel. 08, Created)
 DT 01-NOV-1998 (TREMBrel. 08, Last sequence update)
 DE GLOBULIN-1 (FRAGMENT).
 OS Zea luxurians (Teosinte).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
 OX NCBI_TaxID=15945;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hilton H., Gaut B.S.;
 RT "Speciation and domestication in maize and its wild relatives:
 evidence from the Globulin-1 gene.";
 RL Genetics 0:0-0(1998).
 EMBL; AF064228; AAC31471.1; -.
 HSSP; P50477; ICAU.
 MENDEL; 31899; Zeaau;1188;31899.
 DR INTERPRO; IPR000901; -.
 DR INTERPRO; IPR00113; -.
 DR PPAM; PF00546; Seedstore_7s; 1.
 DR PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
 SQ SEQUENCE 238 AA; 27233 MW; FD31A80666738E68 CRC64;

Query Match 22.7%; Score 80; DB 10; Length 238;
 Best Local Similarity 35.5%; Pred. No. 0/039; Mismatches 18; Indels 16; Gaps 3;

Matches	22;	Conservative	6;	Mismatches	18;	Indels	16;	Gaps	3;
Qy	12	CRRREQQEPROQYQCORRCR-----QQRHGRGDLINPQRGGSG-----RVEEGEE	60						
Db	40	CVRRCEDPRWHQRSRCLQCREFERERKROERSRHA-----RSGEQSSEDERQKEE	94						
Qy	61	KQ 62							
Db	95	KQ 96							

RESULT 15
 Q9ZTP0 PRELIMINARY; PRT; 393 AA.
 ID Q9ZTP0;
 AC Q9ZTP0;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 DE HYPOTHETICAL 45.3 kDa PROTEIN.
 GN OSE705.
 OS Oryza sativa (Rice).
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.
 OC Magnoliophyta; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Oryzaceae; Gramineae; Poaceae; Oryza.
 OX NCBI_TaxID:4530;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=LOMELLO;
 RA Chen P.W., Chen L.J.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF019348; ADD2494.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 393 AA; 45258 MW; DBD019348A2F9E95 CRC64;

Query Match 22.7%; Score 80; DB 10; Length 393;
 Best Local Similarity 31.8%; Pred. No. 0.062; Indels 26; Gaps 4;
 Matches 21; Conservative 7; Mismatches 12;

Qy	6	QREYED-----CRRREQ-----QEQPROQYQCORRC-----REQQRHGRGDLIN	46
Db	67	ORQEQEDDDDDENTHGQGGKBCRRERGQYDRPWKRQECMRQCEWRHEQHHGGC-----	121
Qy	47	PQRGGS 52	
Db	122	--HGGS 125	

Search completed: March 1, 2001, 16:09:17
 Job time: 1561 sec